

SEQUENCE LISTING

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<120> GENE AND PROTEIN SEQUENCES OF PHAGE T4 GENE 35

<130> 8471-007-228

<140> PCT/US99/13024

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<170> PatentIn Ver. 2.0

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Thr Pro Lys Lys Leu Gln Ala Arg Gln Gly Ser Glu Ser Leu Ser Gly		
545	550	555
560		
Ile Val Thr Phe Val Ser Thr Ala Gly Ala Thr Pro Ala Ser Ser Arg		
565	570	575
Glu Leu Asn Gly Thr Asn Val Tyr Asn Lys Asn Thr Asp Asn Leu Val		
580	585	590
Val Ser Pro Lys Ala Leu Asp Gln Tyr Lys Ala Thr Pro Thr Gln Gln		
595	600	605
Gly Ala Val Ile Leu Ala Val Glu Ser Glu Val Ile Ala Gly Gln Ser		
610	615	620
Gln Gln Gly Trp Ala Asn Ala Val Val Thr Pro Glu Thr Leu His Lys		
625	630	635
640		
Lys Thr Ser Thr Asp Gly Arg Ile Gly Leu Ile Glu Ile Ala Thr Gln		
645	650	655
Ser Glu Val Asn Thr Gly Thr Asp Tyr Thr Arg Ala Val Thr Pro Lys		
660	665	670
Thr Leu Asn Asp Arg Arg Ala Thr Glu Ser Leu Ser Gly Ile Ala Glu		
675	680	685
Ile Ala Thr Gln Val Glu Phe Asp Ala Gly Val Asp Asp Thr Arg Ile		
690	695	700
Ser Thr Pro Leu Lys Ile Lys Thr Arg Phe Asn Ser Thr Asp Arg Thr		
705	710	715
720		
Ser Val Val Ala Leu Ser Gly Leu Val Glu Ser Gly Thr Leu Trp Asp		
725	730	735
His Tyr Thr Leu Asn Ile Leu Glu Ala Asn Glu Thr Gln Arg Gly Thr		
740	745	750
Leu Arg Val Ala Thr Gln Val Glu Ala Ala Ala Gly Thr Leu Asp Asn		
755	760	765
Val Leu Ile Thr Pro Lys Lys Leu Leu Gly Thr Lys Ser Thr Glu Ala		
770	775	780
Gln Glu Gly Val Ile Lys Val Ala Thr Gln Ser Glu Thr Val Thr Gly		
785	790	795
800		
Thr Ser Ala Asn Thr Ala Val Ser Pro Lys Asn Leu Lys Trp Ile Ala		
805	810	815
Gln Ser Glu Pro Thr Trp Ala Ala Thr Thr Ala Ile Arg Gly Phe Val		
820	825	830
Lys Thr Ser Ser Gly Ser Ile Thr Phe Val Gly Asn Asp Thr Val Gly		
835	840	845
Ser Thr Gln Asp Leu Glu Leu Tyr Glu Lys Asn Ser Tyr Ala Val Ser		

850	855	860	
Pro Tyr Glu Leu Asn Arg Val Leu Ala Asn Tyr Leu Pro Leu Lys Ala			
865	870	875	880
Lys Ala Ala Asp Thr Asn Leu Leu Asp Gly Leu Asp Ser Ser Gln Phe			
885	890	895	
Ile Arg Arg Asp Ile Ala Gln Thr Val Asn Gly Ser Leu Thr Leu Thr			
900	905	910	
Gln Gln Thr Asn Leu Ser Ala Pro Leu Val Ser Ser Thr Gly Glu			
915	920	925	
Phe Gly Gly Ser Leu Ala Ala Asn Arg Thr Phe Thr Ile Arg Asn Thr			
930	935	940	
Gly Ala Pro Thr Ser Ile Val Phe Glu Lys Gly Pro Ala Ser Gly Ala			
945	950	955	960
Asn Pro Ala Gln Ser Met Ser Ile Arg Val Trp Gly Asn Gln Phe Gly			
965	970	975	
Gly Gly Ser Asp Thr Thr Arg Ser Thr Val Phe Glu Val Gly Asp Asp			
980	985	990	
Thr Ser His His Phe Tyr Ser Gln Arg Asn Lys Asp Gly Asn Ile Ala			
995	1000	1005	
Phe Asn Ile Asn Gly Thr Val Met Pro Ile Asn Ile Asn Ala Ser Gly			
1010	1015	1020	
Leu Met Asn Val Asn Gly Thr Ala Thr Phe Gly Arg Ser Val Thr Ala			
1025	1030	1035	1040
Asn Gly Glu Phe Ile Ser Lys Ser Ala Asn Ala Phe Arg Ala Ile Asn			
1045	1050	1055	
Gly Asp Tyr Gly Phe Phe Ile Arg Asn Asp Ala Ser Asn Thr Tyr Phe			
1060	1065	1070	
Leu Leu Thr Ala Ala Gly Asp Gln Thr Gly Gly Phe Asn Gly Leu Arg			
1075	1080	1085	
Pro Leu Leu Ile Asn Asn Gln Ser Gly Gln Ile Thr Ile Gly Glu Gly			
1090	1095	1100	
Leu Ile Ile Ala Lys Gly Val Thr Ile Asn Ser Gly Gly Leu Thr Val			
1105	1110	1115	1120
Asn Ser Arg Ile Arg Ser Gln Gly Thr Lys Thr Ser Asp Leu Tyr Thr			
1125	1130	1135	
Arg Ala Pro Thr Ser Asp Thr Val Gly Phe Trp Ser Ile Asp Ile Asn			
1140	1145	1150	
Asp Ser Ala Thr Tyr Asn Gln Phe Pro Gly Tyr Phe Lys Met Val Glu			
1155	1160	1165	
Lys Thr Asn Glu Val Thr Gly Leu Pro Tyr Leu Glu Arg Gly Glu Glu			
1170	1175	1180	
Val Lys Ser Pro Gly Thr Leu Thr Gln Phe Gly Asn Thr Leu Asp Ser			

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1185	1190	1195	1200
Leu Tyr Gln Asp Trp Ile Thr Tyr Pro Thr Thr Pro Glu Ala Arg Thr			
1205	1210	1215	
Thr Arg Trp Thr Arg Thr Trp Gln Lys Thr Lys Asn Ser Trp Ser Ser			
1220	1225	1230	
Phe Val Gln Val Phe Asp Gly Gly Asn Pro Pro Gln Pro Ser Asp Ile			
1235	1240	1245	
Gly Ala Leu Pro Ser Asp Asn Ala Thr Met Gly Asn Leu Thr Ile Arg			
1250	1255	1260	
Asp Phe Leu Arg Ile Gly Asn Val Arg Ile Val Pro Asp Pro Val Asn			
1265	1270	1275	1280
Lys Thr Val Lys Phe Glu Trp Val Glu			
1285			

<210> 5
<211> 65
<212> PRT
<213> Bacteriophage T4

<400> 5			
Met Glu Lys Phe Met Ala Glu Ile Trp Thr Arg Ile Cys Pro Asn Ala			
1	5	10	15
Ile Leu Ser Glu Ser Asn Ser Val Arg Tyr Lys Ile Ser Ile Ala Gly			
20	25	30	
Ser Cys Pro Leu Ser Thr Ala Gly Pro Ser Tyr Val Lys Phe Gln Asp			
35	40	45	
Asn Pro Val Gly Ser Gln Thr Phe Arg Arg Arg Pro Ser Phe Lys Ser			
50	55	60	

Phe
65

<210> 6
<211> 295
<212> PRT
<213> Bacteriophage T4

<400> 6			
Met Leu Phe Arg Leu Gln Met Ile Leu His Gln Leu Leu Leu Val			
1	5	10	15
Phe Met Asn Ser Leu Thr Asn Asn Arg Ile Val Ala Ile Leu Thr Ser			
20	25	30	
Gly Lys Val Asn Phe Pro Pro Glu Val Val Ser Trp Leu Arg Thr Ala			
35	40	45	
Gly Thr Ser Ala Phe Pro Ser Asp Ser Ile Leu Ser Arg Phe Asp Val			
50	55	60	
Ser Tyr Ala Ala Phe Tyr Thr Ser Ser Lys Arg Ala Ile Ala Leu Glu			
65	70	75	80

His Val Lys Leu Ser Asn Arg Lys Ser Thr Asp Asp Tyr Gln Thr Ile
 85 90 95

 Leu Asp Val Val Phe Asp Ser Leu Glu Asp Val Gly Ala Thr Gly Phe
 100 105 110

 Pro Arg Arg Thr Tyr Glu Ser Val Glu Gln Phe Met Ser Ala Val Gly
 115 120 125

 Gly Thr Asn Asn Glu Ile Ala Arg Leu Pro Thr Ser Ala Ala Ile Ser
 130 135 140

 Lys Leu Ser Asp Tyr Asn Leu Ile Pro Gly Asp Val Leu Tyr Leu Lys
 145 150 160

 Ala Gln Leu Tyr Ala Asp Ala Asp Leu Leu Ala Leu Gly Thr Thr Asn
 165 170 175

 Ile Ser Ile Arg Phe Tyr Asn Ala Ser Asn Gly Tyr Ile Ser Ser Thr
 180 185 190

 Gln Ala Glu Phe Thr Gly Gln Ala Gly Ser Trp Glu Leu Lys Glu Asp
 195 200 205

 Tyr Val Val Val Pro Glu Asn Ala Val Gly Phe Thr Ile Tyr Ala Gln
 210 215 220

 Arg Thr Ala Gln Ala Gly Gln Gly Met Arg Asn Leu Ser Phe Ser
 225 230 235 240

 Glu Val Ser Arg Asn Gly Gly Ile Ser Lys Pro Ala Glu Phe Gly Val
 245 250 255

 Asn Gly Ile Arg Val Asn Tyr Ile Cys Glu Ser Ala Ser Pro Pro Asp
 260 265 270

 Ile Met Val Leu Pro Thr Gln Ala Ser Ser Lys Thr Gly Lys Val Phe
 275 280 285

 Gly Gln Glu Phe Arg Glu Val
 290 295

<210> 7
 <211> 221
 <212> PRT
 <213> Bacteriophage T4

<400> 7
 Met Ala Asp Leu Lys Val Gly Ser Thr Thr Gly Gly Ser Val Ile Trp
 1 5 10 15

 His Gln Gly Asn Phe Pro Leu Asn Pro Ala Gly Asp Asp Val Leu Tyr
 20 25 30

 Lys Ser Phe Lys Ile Tyr Ser Glu Tyr Asn Lys Pro Gln Ala Ala Asp
 35 40 45

 Asn Asp Phe Val Ser Lys Ala Asn Gly Gly Thr Tyr Ala Ser Lys Val
 50 55 60

 Thr Phe Asn Ala Gly Ile Gln Val Pro Tyr Ala Pro Asn Ile Met Ser

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65	70	75	80
Pro Cys Gly Ile Tyr	Gly Gly Asn Gly Asp	Gly Ala Thr Phe Asp	Lys
85	90	95	
Ala Asn Ile Asp Ile Val Ser Trp	Tyr Gly Val Gly Phe Lys	Ser Ser	
100	105	110	
Phe Gly Ser Thr Gly Arg Thr Val Val Ile Asn Thr Arg Asn Gly Asp			
115	120	125	
Ile Asn Thr Lys Gly Val Val Ser Ala Ala Gly Gln Val Arg Ser Gly			
130	135	140	
Ala Ala Ala Pro Ile Ala Ala Asn Asp Leu Thr Arg Lys Asp Tyr Val			
145	150	155	160
Asp Gly Ala Ile Asn Thr Val Thr Ala Asn Ala Asn Ser Arg Val Leu			
165	170	175	
Arg Ser Gly Asp Thr Met Thr Gly Asn Leu Thr Ala Pro Asn Phe Phe			
180	185	190	
Ser Gln Asn Pro Ala Ser Gln Pro Ser His Val Pro Arg Phe Asp Gln			
195	200	205	
Ile Val Ile Lys Asp Ser Val Gln Asp Phe Gly Tyr Tyr			
210	215	220	

<210> 8
<211> 1026
<212> PRT
<213> Bacteriophage T4

<400> 8			
Met Ala Thr Leu Lys Gln Ile Gln Phe Lys Arg Ser Lys Ile Ala Gly			
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Thr Arg Pro Ala Ala Ser Val Leu Ala Glu Gly Glu Leu Ala Ile Asn			
20	25	30	
Leu Lys Asp Arg Thr Ile Phe Thr Lys Asp Asp Ser Gly Asn Ile Ile			
35	40	45	
Asp Leu Gly Phe Ala Lys Gly Gly Gln Val Asp Gly Asn Val Thr Ile			
50	55	60	
Asn Gly Leu Leu Arg Leu Asn Gly Asp Tyr Val Gln Thr Gly Gly Met			
65	70	75	80
Thr Val Asn Gly Pro Ile Gly Ser Thr Asp Gly Val Thr Gly Lys Ile			
85	90	95	
Phe Arg Ser Thr Gln Gly Ser Phe Tyr Ala Arg Ala Thr Asn Asp Thr			
100	105	110	
Ser Asn Ala His Leu Trp Phe Glu Asn Ala Asp Gly Thr Glu Arg Gly			
115	120	125	
Val Ile Tyr Ala Arg Pro Gln Thr Thr Asp Gly Glu Ile Arg Leu			
130	135	140	

Arg Val Arg Gln Gly Thr Gly Ser Thr Ala Asn Ser Glu Phe Tyr Phe
 145 150 155 160

 Arg Ser Ile Asn Gly Gly Glu Phe Gln Ala Asn Arg Ile Leu Ala Ser
 165 170 175

 Asp Ser Leu Val Thr Lys Arg Ile Ala Val Asp Thr Val Ile His Asp
 180 185 190

 Ala Lys Ala Phe Gly Gln Tyr Asp Ser His Ser Leu Val Asn Tyr Val
 195 200 205

 Tyr Pro Gly Thr Gly Glu Thr Asn Gly Val Asn Tyr Leu Arg Lys Val
 210 215 220

 Arg Ala Lys Ser Gly Gly Thr Ile Tyr His Glu Ile Val Thr Ala Gln
 225 230 235 240

 Thr Gly Leu Ala Asp Glu Val Ser Trp Trp Ser Gly Asp Thr Pro Val
 245 250 255

 Phe Lys Leu Tyr Gly Ile Arg Asp Asp Gly Arg Met Ile Ile Arg Asn
 260 265 270

 Ser Leu Ala Leu Gly Thr Phe Thr Thr Asn Phe Pro Ser Ser Asp Tyr
 275 280 285

 Gly Asn Val Gly Val Met Gly Asp Lys Tyr Leu Val Leu Gly Asp Thr
 290 295 300

 Val Thr Gly Leu Ser Tyr Lys Lys Thr Gly Val Phe Asp Leu Val Gly
 305 310 315 320

 Gly Gly Tyr Ser Val Ala Ser Ile Thr Pro Asp Ser Phe Arg Ser Thr
 325 330 335

 Arg Lys Gly Ile Phe Gly Arg Ser Glu Asp Gln Gly Ala Thr Trp Ile
 340 345 350

 Met Pro Gly Thr Asn Ala Ala Leu Leu Ser Val Gln Thr Gln Ala Asp
 355 360 365

 Asn Asn Asn Ala Gly Asp Gly Gln Thr His Ile Gly Tyr Asn Ala Gly
 370 375 380

 Gly Lys Met Asn His Tyr Phe Arg Gly Thr Gly Gln Met Asn Ile Asn
 385 390 395 400

 Thr Gln Gln Gly Met Glu Ile Asn Pro Gly Ile Leu Lys Leu Val Thr
 405 410 415

 Gly Ser Asn Asn Val Gln Phe Tyr Ala Asp Gly Thr Ile Ser Ser Ile
 420 425 430

 Gln Pro Ile Lys Leu Asp Asn Glu Ile Phe Leu Thr Lys Ser Asn Asn
 435 440 445

 Thr Ala Gly Leu Lys Phe Gly Ala Pro Ser Gln Val Asp Gly Thr Arg
 450 455 460

 Thr Ile Gln Trp Asn Gly Gly Thr Arg Glu Gly Gln Asn Lys Asn Tyr
 465 470 475 480

Val Ile Ile Lys Ala Trp Gly Asn Ser Phe Asn Ala Thr Gly Asp Arg
 485 490 495

 Ser Arg Glu Thr Val Phe Gln Val Ser Asp Ser Gln Gly Tyr Tyr Phe
 500 505 510

 Tyr Ala His Arg Lys Ala Pro Thr Gly Asp Glu Thr Ile Gly Arg Ile
 515 520 525

 Glu Ala Gln Phe Ala Gly Asp Val Tyr Ala Lys Gly Ile Ile Ala Asn
 530 535 540

 Gly Asn Phe Arg Val Val Gly Ser Ser Ala Leu Ala Gly Asn Val Thr
 545 550 555 560

 Met Ser Asn Gly Leu Phe Val Gln Gly Ser Ser Ile Thr Gly Gln
 565 570 575

 Val Lys Ile Gly Gly Thr Ala Asn Ala Leu Arg Ile Trp Asn Ala Glu
 580 585 590

 Tyr Gly Ala Ile Phe Arg Arg Ser Glu Ser Asn Phe Tyr Ile Ile Pro
 595 600 605

 Thr Asn Gln Asn Glu Gly Glu Ser Gly Asp Ile His Ser Ser Leu Arg
 610 615 620

 Pro Val Arg Ile Gly Leu Asn Asp Gly Met Val Gly Leu Gly Arg Asp
 625 630 635 640

 Ser Phe Ile Val Asp Gln Asn Asn Ala Leu Thr Thr Ile Asn Ser Asn
 645 650 655

 Ser Arg Ile Asn Ala Asn Phe Arg Met Gln Leu Gly Gln Ser Ala Tyr
 660 665 670

 Ile Asp Ala Glu Cys Thr Asp Ala Val Arg Pro Ala Gly Ala Gly Ser
 675 680 685

 Phe Ala Ser Gln Asn Asn Glu Asp Val Arg Ala Pro Phe Tyr Met Asn
 690 695 700

 Ile Asp Arg Thr Asp Ala Ser Ala Tyr Val Pro Ile Leu Lys Gln Arg
 705 710 715 720

 Tyr Val Gln Gly Asn Gly Cys Tyr Ser Leu Gly Thr Leu Ile Asn Asn
 725 730 735

 Gly Asn Phe Arg Val His Tyr His Gly Gly Asp Asn Gly Ser Thr
 740 745 750

 Gly Pro Gln Thr Ala Asp Phe Gly Trp Glu Phe Ile Lys Asn Gly Asp
 755 760 765

 Phe Ile Ser Pro Arg Asp Leu Ile Ala Gly Lys Val Arg Phe Asp Arg
 770 775 780

 Thr Gly Asn Ile Thr Gly Gly Ser Gly Asn Phe Ala Asn Leu Asn Ser
 785 790 795 800

 Thr Ile Glu Ser Leu Lys Thr Asp Ile Met Ser Ser Tyr Pro Ile Gly
 805 810 815

Ala Pro Ile Pro Trp Pro Ser Asp Ser Val Pro Ala Gly Phe Ala Leu
820 825 830

Met Glu Gly Gln Thr Phe Asp Lys Ser Ala Tyr Pro Lys Leu Ala Val
835 840 845

Ala Tyr Pro Ser Gly Val Ile Pro Asp Met Arg Gly Gln Thr Ile Lys
850 855 860

Gly Lys Pro Ser Gly Arg Ala Val Leu Ser Ala Glu Ala Asp Gly Val
865 870 875 880

Lys Ala His Ser His Ser Ala Ser Ser Thr Asp Leu Gly Thr
885 890 895

Lys Thr Thr Ser Ser Phe Asp Tyr Gly Thr Lys Gly Thr Asn Ser Thr
900 905 910

Gly Gly His Thr His Ser Gly Ser Gly Ser Thr Ser Thr Asn Gly Glu
915 920 925

His Ser His Tyr Ile Glu Ala Trp Asn Gly Thr Gly Val Gly Gly Asn
930 935 940

Lys Met Ser Ser Tyr Ala Ile Ser Tyr Arg Ala Gly Gly Ser Asn Thr
945 950 955 960

Asn Ala Ala Gly Asn His Ser His Thr Phe Ser Phe Gly Thr Ser Ser
965 970 975

Ala Gly Asp His Ser His Ser Val Gly Ile Gly Ala His Thr His Thr
980 985 990

Val Ala Ile Gly Ser His Gly His Thr Ile Thr Val Asn Ser Thr Gly
995 1000 1005

Asn Thr Glu Asn Thr Val Lys Asn Ile Ala Phe Asn Tyr Ile Val Arg
1010 1015 1020

Leu Ala
1025